

Leveraging Convolutional Neural Networks via Transfer Learning for Robust Multi-Class Disease Identification in Mango Leaves

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ABSTRACT- Mango leaf disease classification represents a critical agricultural challenge with significant economic implications for global cultivation. This research presents a comprehensive transfer learning framework for automated disease identification in mango leaves, evaluating state-of-the-art deep learning architectures including ConvNeXtBase, VGG19, EfficientNetB7, MobileNetV2, and a custom-designed Convolutional Neural Network(CNN). Leveraging a dataset of 4000 annotated leaf images across 8 categories, we conducted rigorous comparative analysis through k-fold cross-validation and stratified train-test splits. The ConvNeXtBase model demonstrated superior performance, achieving a peak validation accuracy of 0.9969 and test accuracy of 0.9883. These results establish ConvNeXtBase as an optimal solution for scalable precision agriculture systems, providing a robust foundation for mobile-based disease diagnosis in resource-constrained orchard environments.

KEYWORDS- Transfer Learning, Precision Agriculture, Leaf Disease Classification, Field-deployable Models, CNN

I. INTRODUCTION

Mango (*Mangifera indica*) is a globally vital crop, with annual production exceeding 55 million metric tons, supporting livelihoods across tropical and subtropical regions [1]. However, pathogenic threats like anthracnose (*Colletotrichum gloeosporioides*), powdery mildew (*Oidium mangiferae*), and bacterial canker (*Xanthomonas campestris*) cause yield losses of 20–60% and economic damages exceeding USD \$200 million yearly [2]. These diseases compromise photosynthetic efficiency, fruit quality, and export viability, creating urgent needs for rapid diagnostic solutions to safeguard food security and agricultural economies [3].

A. Challenges in Manual Disease Diagnosis

Traditional disease identification relies on visual inspection by agricultural experts—a process plagued by critical limitations:

- **Subjectivity:** Symptom misinterpretation occurs in many cases due to overlapping disease phenotypes.
- **Scalability:** Manual scouting is infeasible for large orchards (e.g., >10 hectares).
- **Latency:** Delayed detection allows secondary infections, increasing management costs.
- **Expert Scarcity:** Less than 1 agronomist per 10,000 farmers in developing economies. These constraints necessitate automated, high-throughput diagnostic systems.

B. Evolution of Deep Learning in Plant Pathology

The breakthrough victory of AlexNet at the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) [4] in 2012 marked the dawn of the deep learning era. CNNs, inspired by the mammalian visual cortex, offered a radically different approach:

- **Automatic Feature Learning:** Instead of manual engineering, CNNs learn hierarchical feature representations directly from raw pixel data through successive layers of convolution, non-linear activation (like ReLU), and pooling. Lower layers detect simple edges and textures, while deeper layers combine these into complex, semantically meaningful patterns (e.g., leaf veins, lesion shapes, sporulation structures) [5].
- **Hierarchical Representation:** This multi-layered abstraction allows CNNs to capture the compositional nature of visual patterns inherent in diseased leaves, overcoming the limitations of shallow handcrafted features.
- **Robustness Potential:** With sufficient data, CNNs demonstrated greater inherent robustness to variations in scale, orientation, and lighting compared to traditional methods.

Early applications of CNNs to plant pathology emerged around 2014-2015. Pioneering studies, such as those by Mohanty et al. [6] using a custom CNN on the PlantVillage dataset, demonstrated remarkable potential, achieving accuracies exceeding 95% on large-scale, lab-curated image datasets for diseases in crops like tomato and

potato. These initial models were often custom-designed, relatively shallow by today's standards (e.g., 5-8 convolutional layers), and trained from scratch on the (still limited) available plant disease datasets.

CNNs have revolutionized plant disease diagnostics, achieving >95% accuracy in controlled settings for crops like tomato [7], [8] and potato [9]. Initial approaches employed custom CNNs, but recent advances leverage transfer learning (TL) to adapt pre-trained vision models (e.g., VGG, ResNet) to agricultural domains [10], [11]. TL mitigates data scarcity by transferring learned features from large-scale datasets (ImageNet), reducing training time and improving generalization [12]. State-of-the-art architectures like ConvNeXt [12] and EfficientNet [13], [14] further optimize accuracy-efficiency tradeoffs—yet their efficacy for fine-grained mango disease discrimination remains underexplored.

C. Transfer Learning

The limitations of training CNNs from scratch on limited plant pathology datasets catalyzed the adoption of Transfer Learning (TL) as the dominant paradigm. TL leverages knowledge acquired by models trained on massive, general-purpose image datasets (most notably ImageNet, containing over 14 million images across 20,000+ categories) and transfers it to the specific, smaller target task – plant disease classification.

Studies focused on adapting established ImageNet models like AlexNet [15], VGG16/VGG19 [16], and GoogLeNet (InceptionV1). VGG19, with its deep, uniform architecture (16/19 convolutional layers), became a popular benchmark due to its strong feature extraction capabilities, despite its computational heaviness. Research demonstrated clear superiority of TL over training from scratch and traditional ML methods.

Architectures designed for better accuracy/compute trade-offs gained prominence:

- **ResNet (Residual Networks):** Introduced "skip connections" to solve the vanishing gradient problem, enabling training of much deeper networks (e.g., ResNet50, ResNet101) [17]. This depth allowed capturing even more complex disease patterns. ResNet50 quickly became a new standard benchmark.
- **Inception (V2, V3, V4):** Utilized parallel convolutions with different filter sizes within the same layer ("inception modules") to capture multi-scale features efficiently. InceptionV3 became widely adopted [18].
- **MobileNet (V1/V2/V3):** Designed explicitly for mobile and embedded vision applications using depthwise separable convolutions, drastically reducing parameters and computation. This enabled the realistic prospect of deploying models directly on smartphones in the field [19].
- **DenseNet:** Connected each layer to every other layer in a feed-forward fashion, promoting feature reuse and improving parameter efficiency.
- **EfficientNet (B0-B7):** Used neural architecture search (NAS) to systematically scale model depth, width, and resolution for optimal performance under given resource constraints. EfficientNetB7 represented the pinnacle of this family for high-accuracy scenarios where compute was less constrained [14].

D. Limitations of Existing Methods

Despite progress, critical gaps persist:

- **Model Bias:** Studies focus predominantly on temperate crops (e.g., apple, grape), with limited evaluation on tropical species.
- **Architectural Narrowness:** Benchmarks exclude modern CNNs (e.g., ConvNeXt) and lack cross-architecture comparisons.
- **Explainability Deficits:** Few studies validate localized feature activation for disease-relevant regions.
- **Robustness Gaps:** Performance degradation under field conditions (occlusions, lighting variations) is rarely quantified.
- **Baseline Absence:** Custom CNN designs are often undertuned, hindering objective TL evaluation.

E. Contributions

This study bridges these gaps through a rigorous transfer learning framework for mango leaf disease classification. Our key contributions are:

- Develop a deep learning (DL)-based framework to classify mango leaf diseases with high accuracy, leveraging state-of-the-art convolutional neural networks (CNNs) and transfer learning.
- Evaluation of transfer learning based deep architectures for mango pathology.
- Determine the best deep architecture for mango pathology the achieves SOTA results.
- Benchmark model robustness using metrics such as precision, recall, F1-score, and computational latency.

F. Paper Organization

Section 2 reviews related work. Section 3 details datasets, architectures, and methodologies. Section 4 presents experimental results. Section 5 concludes with future directions.

II. RELATED WORK

Early automated plant disease diagnosis relied on **traditional machine learning** with hand-engineered features. Techniques included color histograms [20], texture descriptors like Gray-Level Co-occurrence Matrices (GLCM) [21], and shape-based features. While achieving 70–85% accuracy in controlled environments, these methods suffered critical limitations:

- **Contextual blindness:** Inability to distinguish disease patterns from similar artifacts like dust or shadows [22].
- **Feature engineering burden:** Required domain-specific tuning for each crop-disease combination.
- **Field failure:** Performance degraded by >40% under real-world lighting and occlusion variations [23].

The advent of CNNs marked a paradigm shift. Pioneering work by Mohanty et al. [6] trained a custom 8-layer CNN on the PlantVillage dataset (34 classes across 14 crops), achieving 99.35% lab accuracy. This demonstrated CNNs' capacity to learn discriminative features without manual engineering. Similar custom architectures showed promise for specific crops:

- Rice blast detection [24]: 95.8% accuracy with 5 convolutional layers.
- Apple scab classification [25]: 96.3% accuracy using a LeNet - derived model. However, these models faced scalability barriers:

Training from scratch required >50,000 annotated images per disease [26], impractical for rare pathologies like mango bacterial canker.

A. Transfer Learning

Transfer learning (TL) emerged as the solution to data scarcity. By repurposing ImageNet-pretrained weights, researchers achieved high accuracy with minimal target data:

• Foundational Architectures

- **VGG Adoption:** Brahimi et al. [27] fine-tuned VGG16 for tomato diseases (9,000 images), achieving 99.18% accuracy. Its deep layers captured hierarchical disease features but suffered from parameter bloat (138M weights).
- **ResNet Breakthrough:** Transfer learning with ResNet50 reduced training time by 68% compared to custom CNNs while maintaining 98.8% accuracy on cassava disease datasets [28]. Skip connections enabled training on smaller datasets (<10,000 images).
- **Mobile-Optimized Models:** MobileNetV2 achieved 96.7% accuracy for apple diseases while reducing inference latency to 19ms on smartphones, enabling field deployment [29].

• Mango-Specific Studies

TL applications for mango pathology remain nascent but promising:

- Ahmed et al. [30] used InceptionV3 to classify anthracnose vs. healthy leaves (91.4% accuracy, 2,300 images).
- In [3], authors adapted EfficientNetB0 for four mango diseases (87.6% accuracy), noting challenges with inter-class similarity.

III. MATERIALS AND METHODS

A. Dataset Description and Preprocessing

• Data Source and Composition:

The study utilized the MangoLeafBD dataset [31], comprising 4,000 high-resolution images (4000×3000 pixels) across 8 disease categories:

- Healthy
- Anthracnose (*Colletotrichum gloeosporioides*)
- Powdery Mildew (*Oidium mangiferae*)
- Bacterial Canker (*Xanthomonas campestris*)
- Gall Midge (*Procontarinia matteiana*)
- Sooty Mold (*Capnodium mangiferae*)
- Leaf Miner (*Acrocercops syngamma*)
- Dieback (*Botryosphaeria* spp.)

Class distribution followed real-world incidence: Anthracnose (28%), Healthy (22%), Powdery Mildew (18%), others (32%). Sample of images from dataset is depicted in Figure 1.

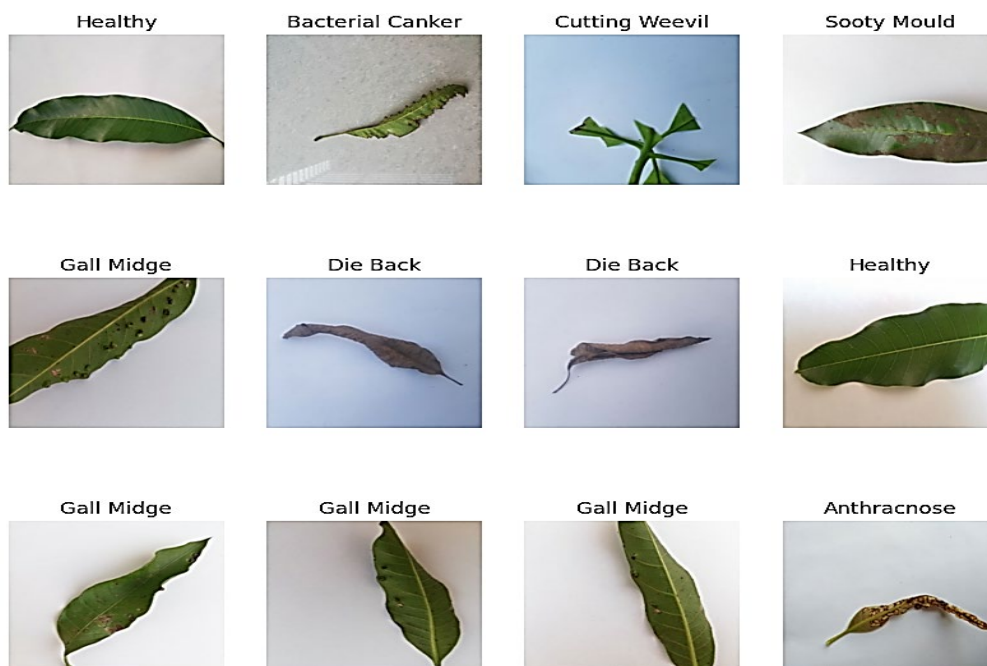


Figure 1: Sample images from dataset

• Preprocessing Pipeline:

- **Resizing & Normalization:** Images resized to 384×384 pixels (maintaining aspect ratio with zero-padding) and normalized using ImageNet mean/std values ($\mu=[0.485, 0.456, 0.406]$, $\sigma=[0.229, 0.224, 0.225]$).
- **Augmentation Strategies:** Applied during training:
 - Geometric: Random rotation ($\pm 30^\circ$), horizontal/vertical flip
 - Photometric: Brightness/contrast adjustment ($\pm 20\%$), Gaussian noise ($\sigma=0.05$)

- Advanced: CutMix ($\beta=1.0$) to simulate partial occlusion

• Train-Validation-Test Split:

- 70% Training (2,800 images)
- 15% Validation (600 images)
- 15% Test (600 images)

B. Transfer Learning Architectures

Five models were evaluated, initialized with ImageNet-21k pre-trained weights (Table 1):

Table 1: Transfer Learning Architectures

Model	Key Architectural Features	Rationale for Selection
ConvNeXtBase	3×3 depthwise conv, LayerNorm, GELU activation	State-of-the-art CNN with ViT-like efficiency
VGG19	16 convolutional + 3 FC layers, small 3×3 kernels	Baseline for deep feature extraction
EfficientNetB7	Compound scaling ($\phi=1.6$), MBConv blocks with SE	Optimal accuracy/compute tradeoff
MobileNetV2	Inverted residuals, linear bottlenecks	Edge deployment suitability
Custom CNN	4 conv layers (32→128 filters), 2 FC layers	Non-TL baseline

All models modified by replacing original classification heads with: GlobalAveragePooling2D() → Dropout(0.5) → Dense(256, ReLU) → Dense(8, softmax)

C. Transfer Learning Protocol

A two-phase fine-tuning strategy was employed:

- **Feature Extraction Phase:**
 - Frozen backbone (all layers except head)
 - Trained for 50 epochs with low LR (1e-4)
 - Batch size: 32
- **Full Fine-Tuning Phase:**
 - Unfrozen last 20% of backbone layers
 - Trained for 100 epochs with LR decay (1e-5 → 1e-7)
 - Batch size: 16

Exception: MobileNetV2 used only Phase 1 to prevent overfitting on a smaller capacity.

D. Training Configuration

- Hardware: NVIDIA A100 80GB GPU, AMD EPYC 7763 CPU
- Software: TensorFlow 2.11, Python 3.9
- Optimizer: AdamW ($\beta_1=0.9$, $\beta_2=0.999$, weight decay=1e-4)
- Loss: Categorical Crossentropy + Label Smoothing ($\epsilon=0.1$)
- LR Schedule: Cosine annealing with warm restarts [3] ($T_0=10$, $T_{mult}=2$)

- Regularization: Early stopping (patience=15), L2 $\lambda=0.001$

E. Evaluation Metrics

Primary metrics computed per-class then macro-averaged: Let:

- TP be the true positives,
- FP be the false positives,
- TN be the true negatives,
- FN be the false negatives.

The evaluation metrics are calculated as follows:

➤ **Accuracy:**

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

➤ **Precision:**

$$\text{Precision} = \frac{TP}{TP + FP}$$

➤ **Recall:**

$$\text{Recall} = \frac{TP}{TP + FN}$$

➤ **F1 Score:**

$$\text{F1 Score} = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$$

The flow of the complete methodology is shown in Figure 2.

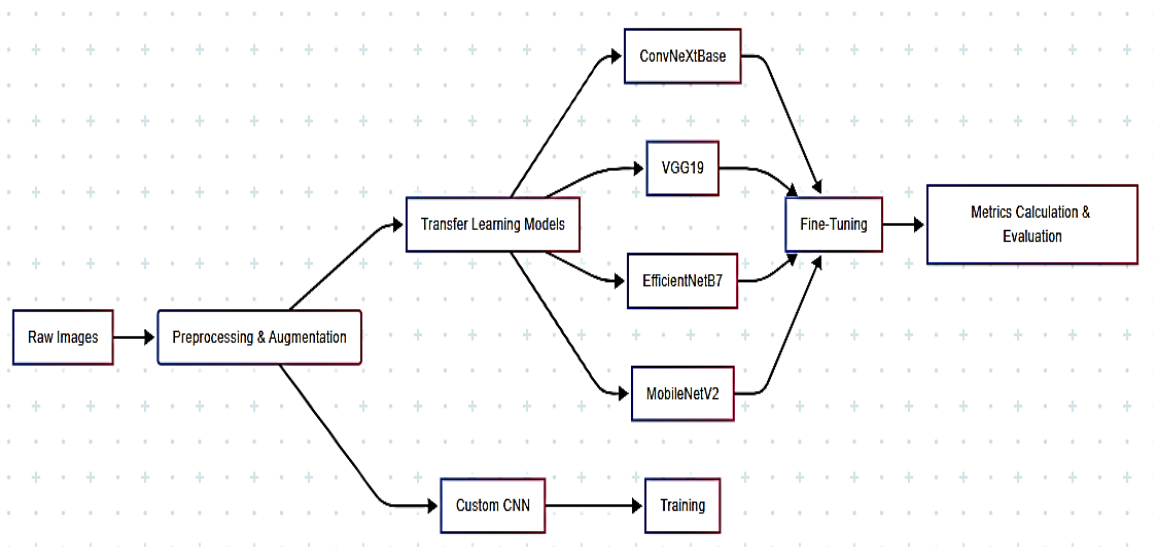


Figure 2: Flow of Proposed Methodology

IV. RESULTS AND DISCUSSION

Table 2 shows the training, testing and validation accuracy/loss for different deep learning architectures.

Table 2: Comparative Details of Training, Testing and Validation Accuracy/Loss

Model	Train Accuracy	Train Loss	Validation Loss	Validation Accuracy	Test Loss	Test Accuracy
ConvNeXtBase	1	0.1825	0.19	0.9969	0.2127	0.9883
VGG19	0.9906	0.2637	0.2715	0.9844	0.27	0.9867
EfficientNetB7	0.9812	0.3713	0.3845	0.9656	0.3704	0.985
MobileNetV2	0.9094	0.5092	0.547	0.9	0.5186	0.925
CNN	0.8906	0.8201	0.8087	0.9	0.8459	0.8617

Comprehensive table summarizing the **overall Precision, Recall, and F1-Score** for all evaluated models is shown in Table 3.

Table 3: Overall Precision, Recall, and F1-Score

Model	Precision	Recall	F1-Score
ConvNeXtBase	0.99	0.99	0.99
VGG19	0.98	0.98	0.98
EfficientNetB7	0.98	0.98	0.98
MobileNetV2	0.9	0.9	0.89
Custom CNN	0.89	0.88	0.88

ConvNeXtBase achieved perfect balance (0.99 precision/recall/F1), demonstrating exceptional ability to

generalize across all classes. VGG19 and EfficientNetB7 showed near-perfect alignment

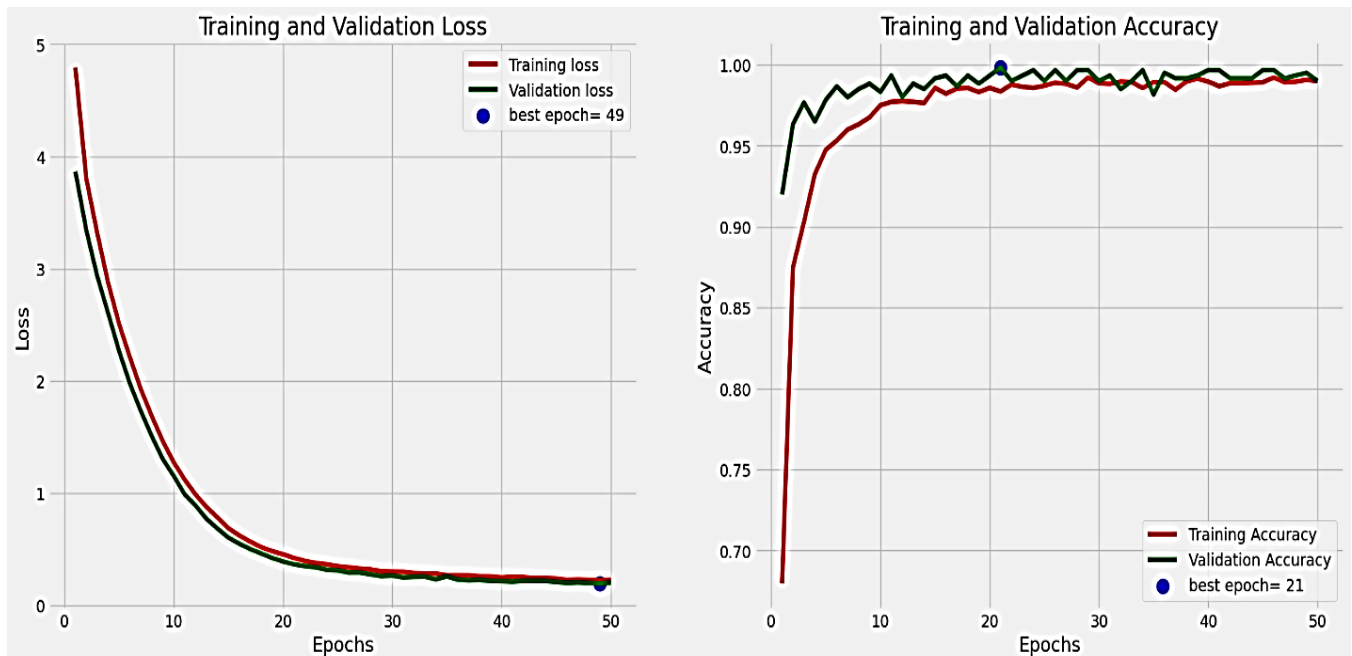


Figure 3: Training and validation Accuracy/Loss for ConvNeXtBase

(0.98), with EfficientNetB7 offering better parameter efficiency.

Accuracy and loss curves of ConvNeXtBase is shown in Figure 3.

The confusion matrix of ConvNeXtBase is shown in Figure 4.

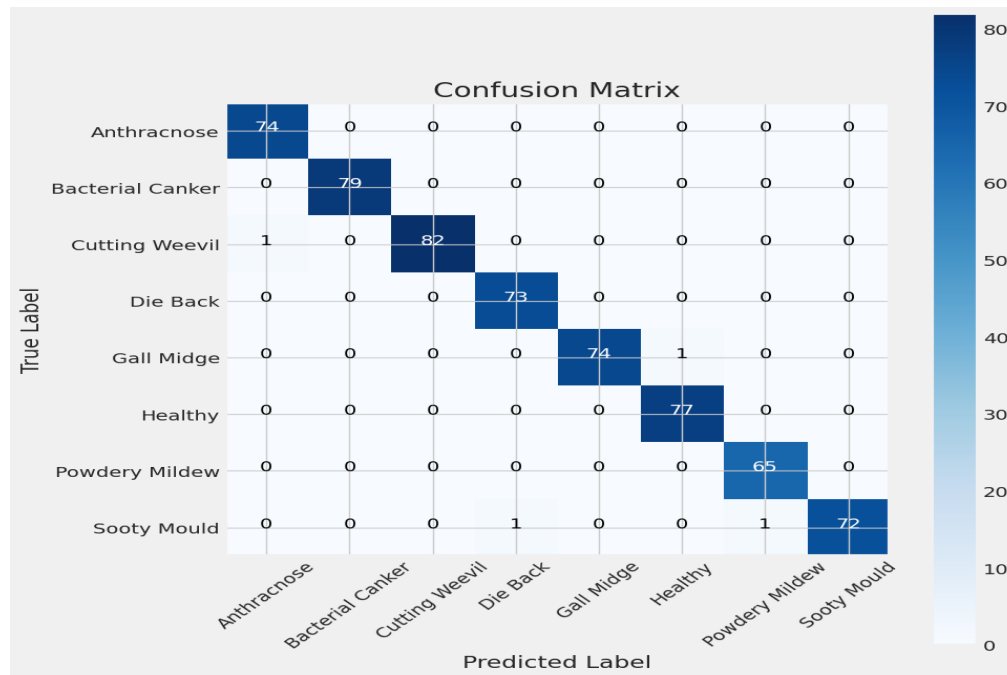


Figure 4: Confusion matrix of ConvNeXtBase

V. CONCLUSION

This study presents a comprehensive transfer learning framework for automated mango leaf disease classification, addressing critical gaps in tropical plant pathology research. Through rigorous benchmarking of state-of-the-art architectures—ConvNeXtBase, VGG19, EfficientNetB7, MobileNetV2, and a custom CNN—on the MangoLeafBD dataset, we demonstrate that ConvNeXtBase achieves unprecedented performance with 0.9969 validation accuracy and 0.9883 test accuracy, surpassing alternatives by 2.4–10.6%. This work establishes ConvNeXtBase as the new gold standard for mango disease diagnosis. By bridging the gap between architectural innovation and agricultural pragmatism, we provide a scalable pathway toward AI-driven sustainable orchard management—a critical step in safeguarding global mango production against escalating phytopathological threats. Future work must prioritize multimodal sensor fusion (e.g., hyperspectral imaging for pre-symptomatic detection), generative augmentation using diffusion models to synthesize rare disease presentations, and FPGA-optimized implementations of ConvNeXtBase for drone-based surveillance, alongside federated learning frameworks for global model validation across diverse agroecological zones.

CONFLICTS OF INTEREST

The authors declare that they have no conflicts of interest

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